1638

#12

RAW SEQUENCE LISTING DATE: 05/29/2001
PATENT APPLICATION: **US/09/308,140** TIME: 11:30:24

Input Set : **A:\F7371c.app**
Output Set: **C:\CRF3\05292001\I308140.raw**


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 3 <110> APPLICANT: BYASS, LOUISE J.
 4       DOUCET, CHARLOTTE J.
 6 <120> TITLE OF INVENTION: CARROT ANTIFREEZE POLYPEPTIDES
 8 <130> FILE REFERENCE: F7371(C)
10 <140> CURRENT APPLICATION NUMBER: 09/308,140
11 <141> CURRENT FILING DATE: 1999-12-30
13 <150> PRIOR APPLICATION NUMBER: PCT/EP97/06181
14 <151> PRIOR FILING DATE: 1997-11-06
16 <150> PRIOR APPLICATION NUMBER: EP 96308362.1
17 <151> PRIOR FILING DATE: 1996-11-19
19 <160> NUMBER OF SEQ ID NOS: 12
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 7
25 <212> TYPE: PRT
26 <213> ORGANISM: Daucus carota
28 <400> SEQUENCE: 1
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30   1               5
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 9
35 <212> TYPE: PRT
36 <213> ORGANISM: Daucus carota
38 <400> SEQUENCE: 2
39 Ile Pro Glu Glu Ile Ser Ala Leu Lys
40   1               5
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 10
45 <212> TYPE: PRT
46 <213> ORGANISM: Daucus carota
48 <220> FEATURE:
49 <221> NAME/KEY: MOD_RES
50 <222> LOCATION: (3)
51 <223> OTHER INFORMATION: any, other or unknown amino acid
53 <400> SEQUENCE: 3
W--> 54 Leu Thr Xaa Leu Asp Leu Ser Phe Asn Lys
55   1               5                  10
58 <210> SEQ ID NO: 4
59 <211> LENGTH: 22
60 <212> TYPE: PRT
61 <213> ORGANISM: Daucus carota
63 <220> FEATURE:
64 <221> NAME/KEY: MOD_RES
65 <222> LOCATION: (21)
66 <223> OTHER INFORMATION: any, other or unknown amino acid
68 <400> SEQUENCE: 4
69 Ser Leu Arg Leu Ser Ser Thr Ser Leu Ser Gly Pro Val Pro Leu Phe
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     70   1               5                  10                  15
W--> 72 Phe Pro Gln Leu Xaa Lys
     73              20
     76 <210> SEQ ID NO: 5
     77 <211> LENGTH: 16
     78 <212> TYPE: PRT
     79 <213> ORGANISM: Daucus carota
     81 <220> FEATURE:
     82 <221> NAME/KEY: MOD_RES
     83 <222> LOCATION: (1)..(16)
     84 <223> OTHER INFORMATION: Xaa represents any, other or unknown amino acid
     86 <400> SEQUENCE: 5
W--> 87 Xaa Xaa Glu Val Ile Pro Xaa Gln Leu Ser Thr Leu Pro Asn Leu Lys
     88   1               5                  10                  15
     91 <210> SEQ ID NO: 6
     92 <211> LENGTH: 999
     93 <212> TYPE: DNA
     94 <213> ORGANISM: Daucus carota
     96 <220> FEATURE:
     97 <221> NAME/KEY: CDS
     98 <222> LOCATION: (1)..(996)
    100 <400> SEQUENCE: 6
    101 atg aat att gaa tca tct ttc tgc cct att ttg tgc ata tgc atg att   48
    102 Met Asn Ile Glu Ser Ser Phe Cys Pro Ile Leu Cys Ile Cys Met Ile
    103   1               5                  10                  15
    105 ttc ctc tgc ctt cca aac ctc tct gca tca caa aga tgc aac aac aac   96
    106 Phe Leu Cys Leu Pro Asn Leu Ser Ala Ser Gln Arg Cys Asn Asn Asn
    107              20                  25                  30
    109 gac aag caa gct tta ctc caa atc aaa aca gcc ttg aaa aac ccc acc   144
    110 Asp Lys Gln Ala Leu Leu Gln Ile Lys Thr Ala Leu Lys Asn Pro Thr
    111          35                  40                  45
    113 att aca gac tca tgg gtg tca gac gac gat tgt tgt ggt tgg gac cta   192
    114 Ile Thr Asp Ser Trp Val Ser Asp Asp Asp Cys Cys Gly Trp Asp Leu
    115      50                  55                  60
    117 gtc gaa tgt gac gaa acc agc aac cgc ata att tcc ctc ata att caa   240
    118 Val Glu Cys Asp Glu Thr Ser Asn Arg Ile Ile Ser Leu Ile Ile Gln
    119  65                  70                  75                  80
    121 gac gac gaa gct ctc acc ggc caa atc cca cct cag gtg gga gac cta   288
    122 Asp Asp Glu Ala Leu Thr Gly Gln Ile Pro Pro Gln Val Gly Asp Leu
    123                  85                  90                  95
    125 cca tac ctc caa gcc tta tgg ttc cgt aaa ctc ccc aat ctt ttc gga   336
    126 Pro Tyr Leu Gln Ala Leu Trp Phe Arg Lys Leu Pro Asn Leu Phe Gly
    127              100                 105                 110
    129 aaa atc cca gaa gaa att tct gca ctc aaa gac cta aaa tcc ctc aga   384
    130 Lys Ile Pro Glu Glu Ile Ser Ala Leu Lys Asp Leu Lys Ser Leu Arg
    131          115                 120                 125
    133 ctc agc tcg acc agt ctc agt ggc cct gtc cct tta ttc ttc cct cag   432
    134 Leu Ser Ser Thr Ser Leu Ser Gly Pro Val Pro Leu Phe Phe Pro Gln
    135      130                 135                 140
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137 ctt acg aaa cta act tgt tta gac tta tcg ttt aac aaa ctt ttg ggt   480
138 Leu Thr Lys Leu Thr Cys Leu Asp Leu Ser Phe Asn Lys Leu Leu Gly
139 145                 150                 155                 160
141 gta atc cct cct cag ctt tcc act ctt ccg aac ctt aaa gcc ctg cac   528
142 Val Ile Pro Pro Gln Leu Ser Thr Leu Pro Asn Leu Lys Ala Leu His
143                 165                 170                 175
145 tta gaa cgt aac gaa ctc acc ggt gaa atc ccc gat atc ttt ggg aat   576
146 Leu Glu Arg Asn Glu Leu Thr Gly Glu Ile Pro Asp Ile Phe Gly Asn
147             180                 185                 190
149 ttt gct gga tcc ccg gac ata tat ctt tcg cat aac cag ctc acc ggg   624
150 Phe Ala Gly Ser Pro Asp Ile Tyr Leu Ser His Asn Gln Leu Thr Gly
151         195                 200                 205
153 ttt gtt ccc aaa act ttt gct aga gca gat cca att agg ctc gac ttc   672
154 Phe Val Pro Lys Thr Phe Ala Arg Ala Asp Pro Ile Arg Leu Asp Phe
155     210                 215                 220
157 tca ggg aac aga cta gaa ggt gat att tca ttc ttg ttt ggg cct aaa   720
158 Ser Gly Asn Arg Leu Glu Gly Asp Ile Ser Phe Leu Phe Gly Pro Lys
159 225                 230                 235                 240
161 aaa cgc ttg gaa atg cta gat ttt tca gga aac gtg ctt agt ttc aat   768
162 Lys Arg Leu Glu Met Leu Asp Phe Ser Gly Asn Val Leu Ser Phe Asn
163                 245                 250                 255
165 ttc tcc agg gtg cag gag ttt cca ccc tct ttg aca tac tta gac ttg   816
166 Phe Ser Arg Val Gln Glu Phe Pro Pro Ser Leu Thr Tyr Leu Asp Leu
167             260                 265                 270
169 aac cat aac cag atc agc gga agt ctg tcg agt gaa ttg gct aaa ttg   864
170 Asn His Asn Gln Ile Ser Gly Ser Leu Ser Ser Glu Leu Ala Lys Leu
171         275                 280                 285
173 gac ctg cag aca ttt aac gtc agt gat aat aat ctc tgc ggc aag att   912
174 Asp Leu Gln Thr Phe Asn Val Ser Asp Asn Asn Leu Cys Gly Lys Ile
175     290                 295                 300
177 cca aca ggg gga aac ctc cag aga ttc gac cgt acg gcc tat ctc cac   960
178 Pro Thr Gly Gly Asn Leu Gln Arg Phe Asp Arg Thr Ala Tyr Leu His
179 305                 310                 315                 320
181 aac agt tgc ttg tgt ggt gct cca ttg cca gaa tgc tag               999
182 Asn Ser Cys Leu Cys Gly Ala Pro Leu Pro Glu Cys
183                 325                 330
186 <210> SEQ ID NO: 7
187 <211> LENGTH: 332
188 <212> TYPE: PRT
189 <213> ORGANISM: Daucus carota
191 <400> SEQUENCE: 7
192 Met Asn Ile Glu Ser Ser Phe Cys Pro Ile Leu Cys Ile Cys Met Ile
193   1               5                  10                  15
195 Phe Leu Cys Leu Pro Asn Leu Ser Ala Ser Gln Arg Cys Asn Asn Asn
196              20                  25                  30
198 Asp Lys Gln Ala Leu Leu Gln Ile Lys Thr Ala Leu Lys Asn Pro Thr
199          35                  40                  45
201 Ile Thr Asp Ser Trp Val Ser Asp Asp Asp Cys Cys Gly Trp Asp Leu
202      50                  55                  60
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204 Val Glu Cys Asp Glu Thr Ser Asn Arg Ile Ile Ser Leu Ile Ile Gln
205  65                  70                  75                  80
207 Asp Asp Glu Ala Leu Thr Gly Gln Ile Pro Pro Gln Val Gly Asp Leu
208                  85                  90                  95
210 Pro Tyr Leu Gln Ala Leu Trp Phe Arg Lys Leu Pro Asn Leu Phe Gly
211             100                 105                 110
213 Lys Ile Pro Glu Glu Ile Ser Ala Leu Lys Asp Leu Lys Ser Leu Arg
214         115                 120                 125
216 Leu Ser Ser Thr Ser Leu Ser Gly Pro Val Pro Leu Phe Phe Pro Gln
217     130                 135                 140
219 Leu Thr Lys Leu Thr Cys Leu Asp Leu Ser Phe Asn Lys Leu Leu Gly
220 145                 150                 155                 160
222 Val Ile Pro Pro Gln Leu Ser Thr Leu Pro Asn Leu Lys Ala Leu His
223                 165                 170                 175
225 Leu Glu Arg Asn Glu Leu Thr Gly Glu Ile Pro Asp Ile Phe Gly Asn
226             180                 185                 190
228 Phe Ala Gly Ser Pro Asp Ile Tyr Leu Ser His Asn Gln Leu Thr Gly
229         195                 200                 205
231 Phe Val Pro Lys Thr Phe Ala Arg Ala Asp Pro Ile Arg Leu Asp Phe
232     210                 215                 220
234 Ser Gly Asn Arg Leu Glu Gly Asp Ile Ser Phe Leu Phe Gly Pro Lys
235 225                 230                 235                 240
237 Lys Arg Leu Glu Met Leu Asp Phe Ser Gly Asn Val Leu Ser Phe Asn
238                 245                 250                 255
240 Phe Ser Arg Val Gln Glu Phe Pro Pro Ser Leu Thr Tyr Leu Asp Leu
241             260                 265                 270
243 Asn His Asn Gln Ile Ser Gly Ser Leu Ser Ser Glu Leu Ala Lys Leu
244         275                 280                 285
246 Asp Leu Gln Thr Phe Asn Val Ser Asp Asn Asn Leu Cys Gly Lys Ile
247     290                 295                 300
249 Pro Thr Gly Gly Asn Leu Gln Arg Phe Asp Arg Thr Ala Tyr Leu His
250 305                 310                 315                 320
252 Asn Ser Cys Leu Cys Gly Ala Pro Leu Pro Glu Cys
253                 325                 330
256 <210> SEQ ID NO: 8
257 <211> LENGTH: 8
258 <212> TYPE: PRT
259 <213> ORGANISM: Daucus carota
261 <400> SEQUENCE: 8
262 Gly Pro Val Pro Leu Phe Phe Pro
263  1               5
266 <210> SEQ ID NO: 9
267 <211> LENGTH: 23
268 <212> TYPE: DNA
269 <213> ORGANISM: Daucus carota
271 <220> FEATURE:
272 <221> NAME/KEY: modified_base
273 <222> LOCATION: (1)..(23)
274 <223> OTHER INFORMATION: "n" represents inosine
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Input Set : A:\F7371c.app
Output Set: C:\CRF3\05292001\I308140.raw

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    276 <400> SEQUENCE: 9
W--> 277 ggnccngtnc cnytnttytt ycc                                          23
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    282 <212> TYPE: DNA
    283 <213> ORGANISM: Daucus carota
    285 <400> SEQUENCE: 10
    286 gagagaggat cctcgagttt ttttttttt tt                                  32
    289 <210> SEQ ID NO: 11
    290 <211> LENGTH: 829
    291 <212> TYPE: DNA
    292 <213> ORGANISM: Daucus carota
    294 <220> FEATURE:
    295 <221> NAME/KEY: CDS
    296 <222> LOCATION: (1)..(591)
    298 <400> SEQUENCE: 11
    299 ggg ccg gtg ccg ctg ttc ttc cct cag ctt acg aaa cta act tgt tta   48
    300 Gly Pro Val Pro Leu Phe Phe Pro Gln Leu Thr Lys Leu Thr Cys Leu
    301   1               5                  10                  15
    303 gac tta tcg ttt aac aaa ctt ttg ggt gta atc cct cct cag ctt tcc   96
    304 Asp Leu Ser Phe Asn Lys Leu Leu Gly Val Ile Pro Pro Gln Leu Ser
    305             20                  25                  30
    307 act ctt ccg aac ctt aaa gcc ctg cac tta gaa cgt aac gaa ctc acc   144
    308 Thr Leu Pro Asn Leu Lys Ala Leu His Leu Glu Arg Asn Glu Leu Thr
    309          35                  40                  45
    311 ggt gaa atc ccc gat atc ttt ggg aat ttt gct gga tcc ccg gac ata   192
    312 Gly Glu Ile Pro Asp Ile Phe Gly Asn Phe Ala Gly Ser Pro Asp Ile
    313      50                  55                  60
    315 tat ctt tcg cat aac cag ctc acc ggg ttt gtt ccc aaa act ttt gct   240
    316 Tyr Leu Ser His Asn Gln Leu Thr Gly Phe Val Pro Lys Thr Phe Ala
    317  65                  70                  75                  80
    319 aga gca gat cca att agg ctc gac ttc tca ggg aac aga cta gaa ggt   288
    320 Arg Ala Asp Pro Ile Arg Leu Asp Phe Ser Gly Asn Arg Leu Glu Gly
    321                 85                  90                  95
    323 gat att tca ttc ttg ttt ggg cct aaa aaa cgc ttg gaa atg cta gat   336
    324 Asp Ile Ser Phe Leu Phe Gly Pro Lys Lys Arg Leu Glu Met Leu Asp
    325             100                 105                 110
    327 ttt tca gga aac gtg ctt agt ttc aat ttc tcc agg gtg cag gag ttt   384
    328 Phe Ser Gly Asn Val Leu Ser Phe Asn Phe Ser Arg Val Gln Glu Phe
    329         115                 120                 125
    331 cca ccc tct ttg aca tac tta gac ttg aac cat aac cag atc agc gga   432
    332 Pro Pro Ser Leu Thr Tyr Leu Asp Leu Asn His Asn Gln Ile Ser Gly
    333     130                 135                 140
    335 agt ctg tcg agt gaa ttg gct aaa ttg gac ctg cag aca ttt aac gtc   480
    336 Ser Leu Ser Ser Glu Leu Ala Lys Leu Asp Leu Gln Thr Phe Asn Val
    337 145                 150                 155                 160
    339 agt gat aat aat ctc tgc ggc aag att cca aca ggg gga aac ctc cag   528
    340 Ser Asp Asn Asn Leu Cys Gly Lys Ile Pro Thr Gly Gly Asn Leu Gln
    341                 165                 170                 175
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PATENT APPLICATION: **US/09/308,140** TIME: 11:30:25

Input Set : **A:\F7371c.app**
Output Set: **C:\CRF3\05292001\I308140.raw**

L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9